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SEQUENCE LISTING Clarke, Lori Connelly, Sheila Ennist, David Forry-Schaudies, Suzanne Gorziglia, Mario Hallenbeck, Paul Hay, Carl Jakubczak, John Kaleko, Michael Phipps, Sandrina Police, Seshidhar Ryan, Patricia Steward, David Xie, Yuefeng <120> Novel Oncolytic Adenoviral Vectors <130> 4-31704A/GTI <140> US 10/081,969 <141> 2002-02-22 US 60/270,922 <150> <151> 2001-02-23 <150> US 60/295,037 <151> 2001-06-01 <150> US 60/348,670 2000-01-14 <151> <160> 98 <170> PatentIn version 3.1 <210> 1 <211> 140 <212> DNA <213> Simian virus 40 <220> <221> misc_feature (1)..(140) <222> <223> <220> <221> misc_feature <222> (1)..(140) <223> Fig. 1 A cttatcgata ccgtcgaaac ttgtttattg cagcttataa tggttacaaa taaagcaaca 120 caaatttcac aaataaagca tttttttcac tgcattctag ttgtggtttg tccaaactca

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                                                                     120
gatgttgcaa gtgtggcgga acacatgtaa gcgacggatg tggcaaaagt gacgtttttg
                                                                     180
gtgtgcgccg gtgtacacag gaagtgacaa ttttcgcgcg gttttaggcg gatgttgtag
                                                                     240
                                                                     300
taaatttggg cgtaaccgag taagatttgg ccattttcgc gggaaaactg aataagagga
agtgaaatct gaataatttt gtgttactca tagcgcgtaa tatttgtcta gggccgcggg
                                                                     360
gactttgacc gtttacgtgg agactcgccc aggtgttttt ctcaggtgtt ttccgcgttc
                                                                     420
cgggtcaaag ttggcgtttt attattatag tcagctgacg tgtagtgtat ttatacccgg
                                                                     480
tgagttcctc aagaggccac tcttgagtgc cagcgagtag agttttctcc tccgagccgc
                                                                     540
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tccgacaccg ggactgaaaa tgagacatat tatctgccac ggaggtgtta ttaccgaaga
<210> 3
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      (1)..(1802)
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       Fig. 3 A-Left end of Ar6pAE2fF sequence
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ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagggcgcga tcaagcttat
                                                                     120
cgataccgtc gaaacttgtt tattgcagct tataatggtt acaaataaag caatagcatc
                                                                     180
acaaatttca caaataaagc attttttca ctgcattcta gttgtggttt gtccaaactc
                                                                     240
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atcaatgtat cttatcatgt ctggatccgc gccgctagcg atcatccgga caaagcctgc 300 360 gegegeeeeg eccegecatt ggeegtaceg cecegegeeg eegeeeeate tegeeeeteg ccgccgggtc cggcgcgtta aagccaatag gaaccgccgc cgttgttccc gtcacggccg 420 gggcagccaa ttgtggcggc gctcggcggc tcgtggctct ttcgcggcaa aaaggatttg 480 qcqcqtaaaa qtqqccqgga ctttgcaggc agcggcggcc gggggcggag cgggatcgag 540 ccctcgatga tatcagatca tcggatcccg gtcgactgaa aatgagacat attatctgcc 600 acggaggtgt tattaccgaa gaaatggccg ccagtctttt ggaccagctg atcgaagagg 660 tactggctga taatcttcca cctcctagcc attttgaacc acctaccctt cacgaactgt 720 atgatttaga cgtgacggcc cccgaagatc ccaacgagga ggcggtttcg cagatttttc 780 ccgactctgt aatgttggcg gtgcaggaag ggattgactt actcactttt ccgccggcgc 840 coggttotoc ggagoogoot cacetttoco ggoagoooga gcagooggag cagagagoot 900 tgggtccggt ttctatgcca aaccttgtac cggaggtgat cgatcttacc tgccacgagg 960 ctggctttcc acccagtgac gacgaggatg aagagggtga ggagtttgtg ttagattatg 1020 tggagcaccc cgggcacggt tgcaggtctt gtcattatca ccggaggaat acgggggacc 1080 cagatattat gtgttcgctt tgctatatga ggacctgtgg catgtttgtc tacagtaagt 1140 gaaaattatg ggcagtgggt gatagagtgg tgggtttggt gtggtaattt tttttttaat 1200 ttttacagtt ttgtggttta aagaattttg tattgtgatt tttttaaaag gtcctgtgtc 1260 tgaacctgag cctgagcccg agccagaacc ggagcctgca agacctaccc gccgtcctaa 1320 aatggcgcct gctatcctga gacgcccgac atcacctgtg tctagagaat gcaatagtag 1380 tacggatage tgtgacteeg gteettetaa cacaceteet gagatacace eggtggteee 1440 gctgtgcccc attaaaccag ttgccgtgag agttggtggg cgtcgccagg ctgtggaatg 1500 tatogaggac ttgcttaacg agcctgggca acctttggac ttgagctgta aacgccccag 1560 gccataaggt gtaaacctgt gattgcgtgt gtggttaacg cctttgtttg ctgaatgagt 1620 tgatgtaagt ttaataaagg gtgagataat gtttaacttg catggcgtgt taaatggggc 1680 ggggcttaaa gggtatataa tgcgccgtgg gctaatcttg gttacatctg acctcatgga 1740 ggcttgggag tgtttggaag atttttctgc tgtgcgtaac ttgctggaac agagctctaa 1800 1802 ca

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tttcccacgt tacgtcactt cccattttaa ttaagaattc tacaattccc aacacataca
                                                                     120
agttactccg ccctaaaacc ctgggcgagt ctccacgtaa acggtcaaag tccccgcggc
                                                                     180
cctagacaaa tattacgcgc tatgagtaac acaaaattat tcagatttca cttcctctta
                                                                     240
ttcagttttc ccgcgaaaat ggccaaatct tactcggtta cgcccaaatt tactacaaca
                                                                     300
teegeetaaa aeegegegaa aattgteact teetgtgtac aeeggegeac aeeaaaaaeg
                                                                     360
tcacttttgc cacatccgtc gcttacatgt gttccgccac acttgcaaca tcacacttcc
                                                                     420
gccacactac tacgtcaccc gccccgttcc cacgccccgc gccacgtcac aaactccacc
                                                                     480
ccctcattat catattggct tcaatccaaa ataaggtata ttattgatga tg
                                                                     532
<210> 5
<211> 660
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                                                                      60
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                                                                     120
atcggatccc ggtcgactga aaatgagaca tattatctgc cacggaggtg ttattaccga
                                                                     180
agaaatggcc gccagtcttt tggaccagct gatcgaagag gtactggctg ataatcttcc
                                                                     240
acctectage cattttgaac cacctaceet teaegaactg tatgatttag aegtgaegge
                                                                     300
ccccgaagat cccaacgagg aggcggtttc gcagattttt cccgactctg taatgttggc
                                                                     360
ggtgcaggaa gggattgact tactcacttt tccgccggcg cccggttctc cggagccgcc
                                                                     420
tcacctttcc cggcagcccg agcagccgga gcagagagcc ttgggtccgg tttctatgcc
                                                                     480
                                                                     540
aaaccttgta ccggaggtga tcgatcttac ctgccacgag gctggctttc cacccagtga
```

```
600
cgacgaggat gaagaggtt aggagtttgt gttagattat gtggagcacc ccgggcacgg
ttgcaggtct tgtcattatc accggaggaa tacgggggac ccagatatta tgtgttcgct
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<210> 6
<211> 660
<212> DNA
<213> Artificial Sequence
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<223> Fig. 5- left end of Ar6pAF sequence
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<223> Fig. 5- left end of Ar6pAF sequence
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                                                                      60
                                                                     120
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cgataccgtc gaaacttgtt tattgcagct tataatggtt acaaataaag caatagcatc
                                                                     180
acaaatttca caaataaagc atttttttca ctgcattcta gttgtggttt gtccaaactc
                                                                     240
                                                                     300
atcaatgtat cttatcatgt ctggatccgc gccgctagcg atatcggatc ccggtcgact
                                                                     360
gaaaatgaga catattatct gccacggagg tgttattacc gaagaaatgg ccgccagtct
tttggaccag ctgatcgaag aggtactggc tgataatctt ccacctccta gccattttga
                                                                     420
accacctacc cttcacgaac tgtatgattt agacgtgacg gcccccgaag atcccaacga
                                                                     480
ggaggcggtt tcgcagattt ttcccgactc tgtaatgttg gcggtgcagg aagggattga
                                                                     540
cttactcact tttccgccgg cgcccggttc tccggagccg cctcaccttt cccggcagcc
                                                                     600
                                                                     660
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                                                                     120
gggctattct aattcaggtt tctctagccg ggctgcagga attcgatggc cgctacctac
                                                                     180
```

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								gtc Val 25								277
								cct Pro								325
	_	_	_			_	_	gac Asp	_		_		_		_	373
	_	_	_	_				ttc Phe			_	_			_	421
	_		_	_	_			gag Glu	_							469
			_		_	_		atg Met 105		_	_			_		517
								gac Asp								565
		_			_	_		aaa Lys			_		_			613
	_	_			cca Pro 150	_		aaa Lys	tgag	ggaag	gcc (cagg	ccag	ct		660
ctg	aatc	cag (cttc	tcag	ac t	gctg	cttt	t gt	gcct	gcgt	aat	gagc	cag (gaact	tcggaa	720
ttt	ctgc	ctt a	aaag	ggac	ca a	gagai	tgtg	g ca	caggi	tagt	cga	atca	agc ·	ttato	cgatac	780
cgt	cgac	ctc q	gact	agat	aa c	ttcg	tata	a tg	tatg	ctat	acga	aagti	tat (gctag	gaaatg	840
gac	ggaat	tta 1	ttac	agag	ca g	cgcc	tgcta	a gaa	aaga	cgca	ggg	cagc	ggc (cgag	caacag	900
cgc	atgaa	atc a	aaga	gctc	ca a	gaca	tggt	t aad	cttg	cacc	agt	gcaa	aa			949
-21	0 > 1	۵														

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<400> 8

Met Ala His Glu Arg Lys Ala Lys Val Leu Arg Arg Met Trp Leu Gln 1 5 10 15

Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu Ser Ala Pro Thr Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His Val Glu Ala Ile Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val Thr Leu Asn Glu 55 Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys Lys Leu Thr Cys Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu Arg Gly Asn Phe Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser Tyr Tyr Gln Thr 105 Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr Gln Val Thr Thr 120 Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu Thr Asp Ile Pro 135 Phe Glu Cys Lys Lys Pro Val Gln Lys 145 <210> 9 <211> 23 <212> DNA <213> Artificial sequence <220> <223> Viral vector sequence <220> <221> misc_feature <222> (1)..(23) <223> Fig. 26a. Sequence of Native E3 region.

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<220>

<400> 9

23

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<211>
      21
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<221> misc_feature
      (1)..(21)
<222>
<223> Fig. 26b(5). Sequence at the junction between E3-6.7 and GM-CSF
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                                                                     21
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<211> 4
<212> PRT
<213> Artificial Sequence
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<223> Fig. 38a. Sequence of native E3-14.5/E3-14.7 junction
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                                                                     23
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                                                                     20
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<211>
      4
<212> PRT
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<223> Viral vector sequence
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                                                                     120
gaaaaaccct cctgcctagg caaaatagca ccctcccgct ccagaacaac atacagcgct
                                                                     180
                                                                     240
tcacagcggc agcctaacag tcagccttac cagtaaaaaa gaaaacctat taaaaaaaaa
                                                                     300
ccactcggat caattcgcgg gggtggccgg ggccagggct tcccacgtgc gcagcaggac
gcagcgctgc ctgaaactcg cgccgcgagg agagggcggg gccgcggaaa ggaaggggag
                                                                     360
                                                                     420
gggctgggag ggcccggagg gggctgggcc ggggacccgg gaggggtcgg gacggggcgg
ggtccgcgcg gaggaggcgg agctggaagg tgaaggggca ggacgggtgc ccgggtcccc
                                                                     480
agteceteeg ceaegtgggg ctaggateet taattaagaa ttetacaatt cecaacacat
                                                                     540
acaagttact ccgccctaaa accctgggcg agtctccacg taaacggtca aagtccccgc
                                                                     600
ggccctagac aaatattacg cgctatgagt aacacaaaat tattcagatt tcacttcctc
                                                                     660
ttattcagtt ttcccgcgaa aatggccaaa tcttactcgg ttacgcccaa atttactaca
                                                                     720
acatecgeet aaaacegege gaaaattgte actteetgtg tacaeeggeg cacaeeaaaa
                                                                     780
acgtcacttt tgccacatcc gtcgcttaca tgtgttccgc cacacttgca acatcacact
                                                                     840
tecgecacae tactaegtea ecegeceegt teccaegeee egegecaegt cacaaactee
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accccctcat tatcatattg gcttcaatcc aaaataaggt atattattga tgatg
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<221> misc_feature
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<220><221><222><222><223>	polyi	_													
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<210><211><212><213>	19 737 DNA Humai	n													
<220><221><222><223>	CDS (108)) (!	539)												
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tattct	aatt (caggi	tttc1	cc ta	aggat	cttt	c ccg	gcago	cagc	eged	cacc		tgg Trp		116
cag ag Gln Se 5															164
gcc cg Ala Ar 20															212
atc ca Ile Gl															260
gag at Glu Me	g aat t Asn	gaa Glu 55	aca Thr	gta Val	gaa Glu	gtc Val	atc Ile 60	tca Ser	gaa Glu	atg Met	ttt Phe	gac Asp 65	ctc Leu	cag Gln	308
gag co Glu Pr															356
cgg gg Arg Gl 85	y Ser			_					_						404
cac ta His Ty 100															452
cag ac															500

ctt gtc atc ccc ttt gac tgc tgg gag cca gtc cag gag tgagtcgaca Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu 135 140	549
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tattacagag cagcgcctgc tagaaagacg cagggcagcg gccgagcaac agcgcatgaa	669
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Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His 20 25 30	
Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp 35 40 45	
Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe 50 55 60	
Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys 65 70 75 80	
Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met 85 90 95	
Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser 100 105 110	
Cys Ala Thr Gln Thr Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys 115 120 125	
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taaaaaaaca ccactcggat caattcgcgg gggtggccgg ggccagggct tcccacgtgc
                                                                     120
gcagcaggac gcagcgctgc ctgaaactcg cgccgcgagg agagggcggg gccgcggaaa
                                                                     180
aggaacggga cgggctggga tggcccggaa ggggctgggc cggggacccg ggaagggttc
                                                                     240
gggacgggc ggggttccgc gcggacgagg cggagctgga aggtgaaggg gcaggaccgg
                                                                     300
tgcccgggtc cccagtccct ccgccacgtg gggctaggat ccttaattaa gaattctaca
                                                                     360
                                                                     403
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<223> E1A Forward primer
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                                                                      21
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gtcatcttgg gtggcgaccc cagc
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gaaaaacacg ataataccat ggcccacgag agaaagg
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<211> 25
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<211> 44
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<223> Table.27. 147BH primer sequence
<220>
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<400> 58
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gcagccacat ggtcagtcgt ctcctcctgt tagattaaag tagc
<210> 59
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                                                                     45
<210> 60
<211> 44
<212> DNA
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geecea	teat teteteat tactorigga teggeteeta goag	
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ccagga	gtaa taaaaaaaa taataaagca tcac	34
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	(1)(26)	
	Table 27. 147F primer sequence	
	•	
	62	2.0
ggccgt	tgcc cattttgagc gcaagc	26
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	(1)(45)	
	Table 27. Ar16.1	
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<223> Table 27. 147DH primer sequence

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<400> 65
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                                                                     28
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<400> 66
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agcaggaggg aacagagctg ttaggaagc
<210> 67
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<400> 68
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<400> 69
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<400> 73
ggcgtgaccg taaaaaaact ggtcaccgtg at
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<210> 74
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<400> 74
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cacataaaca cctgaaaaac cctcctgcc
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<211> 29
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333						
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12237	VIIII VOODOI BOQUOMOC					
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	(1)(25)					
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-4005	02					
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ccacac	geac acceegggee aggae	23				
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	A 397 bp fragment of the hTERT promoter					
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		120				
ccagac	cccc gggtccgccc ggagcagctg cgctgtcggg gccaggccgg gctcccagtg	120				
gattcg	cggg cacagacgcc caggaccgcg cttcccacgt ggcggaggga ctggggaccc	180				
J 2 5		-				
gggcac	ccgt cctgcccctt caccttccag ctccgcctcc tccgcgcgga ccccgccccg	240				
tcccga	cccc teeegggtee ceggeecage eeeeteeggg eeeteecage eeeteeeett	300				

.

```
cettteegeg geoegeest etectegegg egegagttte aggeageget gegteetget
                                                                    360
                                                                    397
gcgcacgtgg gaagccctgg ccccggccac ccccgcg
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<223> A 245 bp fragment of the hTERT promoter
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                                                                     60
                                                                    120
cogcetecte egogoggace ecgeceegte ecgaceete eegggteece ggeceageee
ceteegggee eteceageee eteceettee ttteegegge eeegeeetet eetegeggeg
                                                                    180
cgagtttcag gcagcgctgc gtcctgctgc gcacgtggga agccctggcc ccggccaccc
                                                                    240
                                                                    245
ccgcg
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cttcgatgat gccgcagtg
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<400>	98 ccaa gataaccatg	20